

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/528,928
Source: PCT
Date Processed by STIC: 4-6-05

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/528, 928

CRF Edit Date: 4-6-05
Edited by: ze

☒ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

☐ Corrected the SEQ ID NO. Sequence numbers edited were:

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☒ Deleted: ☒ invalid beginning/end-of-file text ; _____ page numbers

☐ Inserted mandatory headings/numeric identifiers, specifically:

☐ Moved responses to same line as heading/numeric identifier, specifically:

☐ Other:



PCT

RAW SEQUENCE LISTING

DATE: 04/06/2005

PATENT APPLICATION: US/10/528,928

TIME: 15:30:37

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\04062005\J528928.raw

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9 <110> APPLICANT: Janssen Pharmaceutica N.V.
11 <120> TITLE OF INVENTION: Amyloid-Beta monoclonal antibodies, compositions, methods
and uses
13 <130> FILE REFERENCE: PRD 32
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/528,928
C--> 15 <141> CURRENT FILING DATE: 2005-03-23
15 <150> PRIOR APPLICATION NUMBER: PCT/EP02/11062
16 <151> PRIOR FILING DATE: 2002-09-27
18 <160> NUMBER OF SEQ ID NOS: 12
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 5
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Immunogen consisting of the first 5 amino acids of the BACE1
clea
29      vage site of human amyloid beta
31 <400> SEQUENCE: 1
33 Glu Val His His Gln
34 1      5
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 7
39 <212> TYPE: PRT
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Immunogen consisting of the first 7 amino acids of the BACE1
clea
44      vage site of human amyloid beta
46 <400> SEQUENCE: 2
48 Glu Val His His Gln Lys Ile
49 1      5
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 5
54 <212> TYPE: PRT
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: Immunogen consisting of the first 5 amino acids of the BACE1
clea
59      vage site of mouse amyloid beta
61 <400> SEQUENCE: 3
63 Glu Val Arg His Gln
64 1      5
67 <210> SEQ ID NO: 4

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68 <211> LENGTH: 7
69 <212> TYPE: PRT
70 <213> ORGANISM: Artificial Sequence

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72 <220> FEATURE:
73 <223> OTHER INFORMATION: Immunogen consisting of the first 7 amino acids of the BACE1
clea
74     vage site of mouse amyloid beta
76 <400> SEQUENCE: 4
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79 1         5
82 <210> SEQ ID NO: 5
83 <211> LENGTH: 136
84 <212> TYPE: PRT
85 <213> ORGANISM: Mus sp.
87 <220> FEATURE:
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89 <222> LOCATION: (50)..(54)
90 <223> OTHER INFORMATION:
93 <220> FEATURE:
W--> 94 <221> NAME/KEY: CDR2
95 <222> LOCATION: (69)..(85)
96 <223> OTHER INFORMATION:
W--> 99 <220>
W--> 100 <221> NAME/KEY: CDR3
101 <222> LOCATION: (118)..(125)
102 <223> OTHER INFORMATION:
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107 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Ile Gly
108 1         5         10         15
111 Ile Asn Ser Glu Gly Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
112         20         25         30
115 Ser Gly Ala Ser Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
116         35         40         45
119 Lys Asp His Tyr Val His Trp Val Arg Gln Arg Pro Glu Gln Gly Leu
120         50         55         60
123 Asp Trp Ile Gly Trp Ile Ala Pro Lys Asn Gly Tyr Ser Glu Ser Ala
124 65         70         75         80
127 Pro Lys Phe Gln Gly Lys Ala Ser Met Thr Ala Asp Thr Ser Ser Asn
128         85         90         95
131 Thr Val Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
132         100        105        110
135 Tyr Tyr Cys Phe Ala Gly Phe Tyr Asp Ser Ser Leu Tyr Trp Gly Gln
136         115        120        125
139 Gly Thr Thr Leu Thr Val Ser Ser
140         130        135
143 <210> SEQ ID NO: 6
144 <211> LENGTH: 133
145 <212> TYPE: PRT
146 <213> ORGANISM: Mus sp.
148 <220> FEATURE:
W--> 149 <221> NAME/KEY: CDR1
150 <222> LOCATION: (44)..(59)
151 <223> OTHER INFORMATION:

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154 <220> FEATURE:
W--> 155 <221> NAME/KEY: CDR2
156 <222> LOCATION: (75)..(81)
157 <223> OTHER INFORMATION:
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W--> 161 <221> NAME/KEY: CDR3
162 <222> LOCATION: (114)..(122)
163 <223> OTHER INFORMATION:
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169 1 5 10 15
172 Glu Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ala
173 20 25 30
176 Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Gly Gln Ser
177 35 40 45
180 Leu Leu Ala Arg Asp Gly Lys Thr Tyr Leu Ser Trp Leu Leu Gln Arg
181 50 55 60
184 Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
185 65 70 75 80
188 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
189 85 90 95
192 Thr Leu Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr
193 100 105 110
196 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Asn
197 115 120 125
200 Leu Glu Ile Lys Arg
201 130
204 <210> SEQ ID NO: 7
205 <211> LENGTH: 133
206 <212> TYPE: PRT
207 <213> ORGANISM: Mus sp.
209 <220> FEATURE:
W--> 210 <221> NAME/KEY: CDR1
211 <222> LOCATION: (50)..(54)
212 <223> OTHER INFORMATION:
215 <220> FEATURE:
W--> 216 <221> NAME/KEY: CDR2
217 <222> LOCATION: (69)..(85)
218 <223> OTHER INFORMATION:
W--> 221 <220>
W--> 222 <221> NAME/KEY: CDR3
223 <222> LOCATION: (118)..(122)
224 <223> OTHER INFORMATION:
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229 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
230 1 5 10 15
233 Val Leu Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
234 20 25 30
237 Pro Gly Ala Ser Val Lys Thr Ser Cys Lys Thr Ser Gly Tyr Ser Phe

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238          35          40          45
241 Thr Glu Tyr Ile Met Ser Trp Val Arg Gln Ser His Gly Lys Ser Leu
242          50          55          60
245 Glu Trp Ile Gly Ser Ile Asn Pro Asn Thr Gly Gly Ser Arg Tyr Asn
246 65          70          75          80
249 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
250          85          90          95
253 Thr Ala Tyr Met Glu Phe Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
254          100          105          110
257 Tyr Tyr Cys Ala Arg Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr
258          115          120          125
261 Leu Thr Val Ser Ser
262          130
265 <210> SEQ ID NO: 8
266 <211> LENGTH: 133
267 <212> TYPE: PRT
268 <213> ORGANISM: Mus sp.
270 <220> FEATURE:
W--> 271 <221> NAME/KEY: CDR1
272 <222> LOCATION: (44)..(59)
273 <223> OTHER INFORMATION:
276 <220> FEATURE:
W--> 277 <221> NAME/KEY: CDR2
278 <222> LOCATION: (75)..(81)
279 <223> OTHER INFORMATION:
W--> 282 <220>
W--> 283 <221> NAME/KEY: CDR3
284 <222> LOCATION: (114)..(122)
285 <223> OTHER INFORMATION:
W--> 288 <400> 8
290 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
291 1          5          10          15
294 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
295          20          25          30
298 Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Asn
299          35          40          45
302 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Arg
303          50          55          60
306 Pro Gly Gln Ser Pro Gln Leu Leu Ile Ser Arg Val Ser Asn Leu Ala
307 65          70          75          80
310 Ser Gly Val Pro Asn Arg Phe Ser Gly Ser Glu Ser Gly Thr Asp Phe
311          85          90          95
314 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
315          100          105          110
318 Cys Ala Gln Leu Leu Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys
319          115          120          125
322 Leu Glu Ile Lys Arg
323          130
326 <210> SEQ ID NO: 9

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Input Set : A:\pto.kd.txt

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327 <211> LENGTH: 138
328 <212> TYPE: PRT
329 <213> ORGANISM: Mus sp.
331 <220> FEATURE:
W--> 332 <221> NAME/KEY: CDR1
333 <222> LOCATION: (50)..(54)
334 <223> OTHER INFORMATION:
337 <220> FEATURE:
W--> 338 <221> NAME/KEY: CDR2
339 <222> LOCATION: (69)..(85)
340 <223> OTHER INFORMATION:
W--> 343 <220>
W--> 344 <221> NAME/KEY: CDR3
345 <222> LOCATION: (118)..(127)
346 <223> OTHER INFORMATION:
W--> 349 <400> 9
351 Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
352 1 5 10 15
355 Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys
356 20 25 30
359 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe
360 35 40 45
363 Ser Thr Ser Trp Ile Glu Trp Ile Lys Gln Arg Pro Gly His Gly Leu
364 50 55 60
367 Glu Trp Ile Gly Glu Val Leu Pro Gly Ser Gly Lys Ser Asn His Asn
368 65 70 75 80
371 Ala Asn Phe Lys Gly Arg Ala Thr Phe Thr Ala Asp Thr Ala Ser Asn
372 85 90 95
375 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
376 100 105 110
379 Tyr Tyr Cys Ala Arg Glu Gly Ser Asn Asn Asn Ala Leu Ala Tyr Trp
380 115 120 125
383 Gly Gln Gly Thr Leu Val Thr Val Ser Ala
384 130 135
387 <210> SEQ ID NO: 10
388 <211> LENGTH: 128
389 <212> TYPE: PRT
390 <213> ORGANISM: Mus sp.
392 <220> FEATURE:
W--> 393 <221> NAME/KEY: CDR1
394 <222> LOCATION: (46)..(55)
395 <223> OTHER INFORMATION:
398 <220> FEATURE:
W--> 399 <221> NAME/KEY: CDR2
400 <222> LOCATION: (60)..(67)
401 <223> OTHER INFORMATION:
W--> 404 <220>
W--> 405 <221> NAME/KEY: CDR3
406 <222> LOCATION: (110)..(117)

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/528,928

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Input Set : A:\pto.kd.txt

Output Set : N:\CRF4\04062005\J528928.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:88 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:94 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:99 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:90
L:100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:105 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:96
L:105 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:102
L:149 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:155 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:160 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:151
L:161 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:166 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:157
L:166 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:163
L:210 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:216 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:221 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:212
L:222 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:227 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:218
L:227 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:224
L:271 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:277 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:282 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:273
L:283 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
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L:288 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:285
L:332 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:338 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:343 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:334
L:344 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:349 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:340
L:349 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:346
L:393 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:399 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:404 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:395
L:405 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:410 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:401
L:410 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:407
L:450 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:456 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:461 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:452
L:462 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:467 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:458
L:467 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:464
L:511 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
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L:522 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:513
L:523 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12

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L:528 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:525